AMENDMENTS TO THE CLAIMS

1. **(Currently Amended)** A method of identifying at least one epitope binding domain capable of binding to a predetermined epitope comprising:

(a) displaying on the surface of a biological display system a panel of ~~bivalent or multivalent~~ recombinant polypeptides comprised of (1) an N-terminal blocking domain at the N-terminus of said recombinant polypeptide, (2) a C-terminal anchoring domain at the C-terminus of said recombinant polypeptide, said C-terminal anchoring domain ~~that~~ mediates anchoring of said recombinant polypeptide to the surface of said display system, and (3) at least one epitope binding domain positioned between said N-terminal blocking domain and said C-terminal anchoring domain; and

(b) identifying a subset of said recombinant polypeptides that bind to said predetermined epitope.

2. **(Currently Amended)** The method of claim 1, wherein said N-terminal blocking domain and said epitope binding domain are linked by a polypeptide linker, ~~wherein said polypeptide linker comprises a plurality of hydrophilic amino acids and connects the C-terminal end of said blocking domain and the N-terminal end of said epitope binding domain~~.

3. **(Previously Presented)** The method of claim 1 or 2, wherein said epitope binding domain is a pair of V_H-V_L, V_H-V_H or V_L-V_L domains.

4. **(Currently Amended)** The method of claim 1 wherein said display system is a filamentous phage system ~~produced by bacteria transfected therewith~~, a baculovirus expression system, a ribosome based expression system, a bacteriophage lambda display system or a bacterial surface expression system.

5. **(Currently Amended)** The method of claim 4, further comprising, prior to step (a),

the further step of:

(a") transfecting bacteria with recombinant vectors encoding said recombinant polypeptides.

6. **(Currently Amended)** The method of claim ~~1-~~5, further comprising, prior to step (a"), the further step of:

(a') cloning a panel of nucleic acid molecules encoding said epitope binding domain into a vector.

7. **(Original)** The method of claim 6, wherein said panel of nucleic acid molecules is derived from immune competent cells of a mammal, fish or bird.

8. **(Currently Amended)** The method of claim 1, wherein said N-terminal ~~binding~~ blocking domain comprises at least 9 amino acids.

9. **(Currently Amended)** The method of claim 8, wherein said ~~C-terminal anchoring~~N-terminal blocking domain is or is derived from the N2-domain of the gene III product of filamentous phage.

10. **(Previously Presented)** The method of claim 1, wherein said C-terminal anchoring domain is or is derived from the C-terminal CT-domain of the gene III product of filamentous phage.

11. **(Currently Amended)** The method of claim 1, wherein said ~~bi- or multivalent~~ recombinant polypeptide is a bi- or multifunctional polypeptide.

12. **(Currently Amended)** The method of claim 1, wherein said N-terminal blocking domain comprises an amino acid sequences that forms an effector ~~protein~~ domain having a ~~conformation suitable for~~ a biological activity~~, capable of sequestering an ion, or capable of selective binding to a solid support~~.

13. **(Currently Amended)** The method of claim 12 wherein said effector ~~protein~~ domain is an enzyme, toxin, receptor, binding site, biosynthetic antibody binding site, growth factor, cell-differentiation factor, lymphokine, cytokine or hormone.

14. **(Currently Amended)** The method of claim ~~12~~ 38 wherein said sequence capable of sequestering an ion is calmodulin, methallothionein, a fragment thereof, or an amino acid sequence rich in at least one of glutamic acid, aspartic acid, lysine, and arginine.

15. **(Currently Amended)** The method of claim ~~12~~38 wherein said polypeptide sequence capable of selective binding to a solid support is a positively or negatively charged amino acid sequence, a cysteine-containing amino acid sequence, streptavidin, or a fragment of Staphylococcus protein A.

16. **(Currently Amended)** The method of claim 13, wherein said receptor ~~is~~comprises a co-stimulatory surface molecule important for T-cell activation, ~~or comprises~~ an epitope binding domain~~site~~ or a hormone binding site.

17. **(Original)** The method of claim 16, wherein said co-stimulatory surface molecule is CD80 (B7-1), CD86 (B7-2), CD58 (LFA-3) or CD54 (ICAM-1).

18. **(Cancelled)**

19. **(Currently Amended)** The method of claim 3, wherein said pair of epitope binding domains are connected by a flexible linker. ~~, preferably by a polypeptide linker disposed between said domains, wherein said polypeptide linker comprises a plurality of hydrophilic amino acids of a length sufficient to span the distance between the C-terminal end of one of said domains and the N-terminal end of the other of said domains when said fusion protein assumes a conformation suitable for binding when disposed in aqueous solution.~~

20. **(Currently Amended)** The method of claim 1, ~~wherein the identification of said~~further comprising the ~~binding site domain comprises the~~ steps of:

~~(b') removing said anchoring domain from said recombinant polypeptide;~~

~~(b") periplasmatically expressing the nucleic acid molecules encoding the remainder of said recombinant polypeptide in bacteria; and~~

(b"') verifying whether said epitope binding ~~site~~ domain binds to said predetermined epitope.

21. **(Currently Amended)** ~~K~~A kit comprising:

(a) a panel of recombinant vectors encoding a panel of recombinant polypeptides comprised of: ~~as defined in any one of claims 1 to 20; and/or~~

i. an N-terminal blocking domain at the N-terminus of said recombinant polypeptides;

ii. a C-terminal anchoring domain at the C-terminus of said recombinant polypeptides;

iii. at least one epitope binding domain positioned between said N-terminal blocking domain and said C-terminal anchoring domain; and

(b) a bacterial library transfected with a panel of vectors as defined in (a).

22. **(Currently Amended)** An isolated epitope binding ~~site~~ domain or recombinant polypeptide obtainable by the method of claim 1, wherein said epitope binding ~~site~~ domain or recombinant polypeptide comprises at least ~~one~~ three of the complementarity determining regions (CDR) ~~of the scFv fragment according to any one of~~ from SEQ ID Nos. 61, 63, 65, 67, 69, 71, 73, 75 and 77.

23. **(Currently Amended)** An isolated polypeptide or ~~an~~ antibody comprising at least one epitope binding ~~site~~ domain ~~or fusion protein of~~ according to claim 22.

24. **(Currently Amended)** ~~The~~An isolated polypeptide or antibody ~~of claim 23 having~~comprising at least one epitope binding domain selected from the group consisting

of ~~the amino acid sequence according to any one of~~ SEQ ID Nos.~~:~~ 61, 63, 65, 67, 69, 71, 73, 75 and 77.

25. **(Currently Amended)** An isolated ~~P~~polynucleotides ~~which upon expression~~ that encodes ~~the~~ a polypeptide or antibody ~~of~~ according to claim 23 or 24.

26. **(Currently Amended)** A cell transfected with a polynucleotide ~~of~~according to claim 25.

27. **(Original)** A process for the preparation of a polypeptide or antibody of claim 23 or 24 comprising cultivating a cell of claim 26 under conditions suitable for the expression of the polypeptide and isolating the polypeptide from the cell culture medium.

28. **(Currently Amended)** A pharmaceutical composition ~~containing~~comprising a polypeptide or antibody ~~of~~according to claim 23 or 24 ~~and optionally a pharmaceutically acceptable carrier~~.

29. **(Currently Amended)** A diagnostic composition comprising the polypeptide or antibody of claim 23 or 24~~ and optionally suitable means for detection~~.

30. **(Currently Amended)** An isolated epitope binding ~~site~~ domain or recombinant polypeptide obtainable by the method of claim 1, wherein said epitope binding ~~site~~ domain or recombinant polypeptide comprises ~~at least one~~ the three complementarity determining regions (CDR) ~~of the scFv fragment according to~~ from SEQ ID No. 75.

31. **(Currently Amended)** An isolated polypeptide or ~~an~~ antibody comprising at least one epitope binding ~~site~~ domain or recombinant polypeptide ~~of~~ according to claim 30.

32. **(Currently Amended)** ~~The~~An isolated polypeptide or antibody ~~of claim 23, having~~ comprising the amino acid sequence ~~according to~~ set forth in SEQ ID No. 75.

33. **(Currently Amended)** The polypeptide of claim 32 ~~having~~ comprising the amino acid sequence ~~according to~~set forth in SEQ ID No. 75.

34. **(Currently Amended)** An isolated polypeptide or an antibody comprising at least ~~one~~three of the complementarity binding regions (CDR)~~binding site domain or recombinant polypeptide that comprises any one of~~ from SEQ ID Nos. 61, 63, 65, 67, 69, 71, 73, 75 and 77.

35. **(Currently Amended)** An isolated polypeptide or an antibody comprising ~~at least one~~ the epitope binding ~~site~~ domain ~~or fusion protein that comprises~~set forth in SEQ ID No. 75.

36. **(Previously Presented)** The method of claim 1, wherein said epitope binding domain is comprised of at least two domains selected from the group consisting of V_H and V_L.

37. **(Previously Presented)** The method of claim 19, wherein said polypeptide linker comprises a plurality of hydrophilic amino acids and allows for said epitope binding domains to assume a conformation suitable for binding epitope when disposed in aqueous solution.

38. **(New)** The method of claim 12, wherein said effector protein domain is capable of sequestering an ion or selective binding to a solid support.

39. **(New)** The pharmaceutical composition according to claim 28, further comprising a pharmaceutically acceptable carrier.

40. **(New)** The diagnostic composition according to claim 29, further comprising means for detection.

41. **(New)** The method of claim 1, wherein said recombinant polypeptides are bivalent or multivalent.

42. (**New**) The method of claim 2, wherein said polypeptide linker comprises a plurality of hydrophilic amino acids and connects the C-terminal end of said blocking domain and the N-terminal end of said epitope binding domain